SEQUENCE LISTING

<110> Cowsert, Lex M.
Baker, Brenda F.
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Freier, Susan M.
Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
Wyatt, Jacqueline R.
Borchers, Alexander
Vickers, Timothy A.

<120> Identification of Genetic Targets for Modulation by Oligonucleotides and Generation of Oligonucleotides for Gene Modulation

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Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe
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Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His Lys Tyr Cys
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Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr
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Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
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Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser
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125 130 135

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Arg Ser Glu Glu Gly Arg Asp Met Ala Asn Arg Ile Ser Ala Phe Gly
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Tyr Leu Glu Cys Ser Ala Lys Thr Lys Glu Gly Val Arg Glu Val Phe
160 165 170

gag atg gcc act cgg gct ggc ctc cag gtc cgc aag aac aag cgt cgg 637
Glu Met Ala Thr Arg Ala Gly Leu Gln Val Arg Lys Asn Lys Arg Arg
175 180 185

agg ggc tgt ccc att ctc tga gatcccccca aagggccctt ttcctacatg 688
Arg Gly Cys Pro Ile Leu
190

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aacatattct gaatattttt gctgtgaaac acttgacagc agagctttcc accatgaaaa 300

gaagcttcat gagtcacaca ttacatcttt gggttgattg aatgccactg aaacattcta 360

gtagcctgga gaagttgacc tacctgtgga gatgcctgcc attaaatggc atcctgatgg 420

cttaatacac atcactcttc tgtgaagggt tttaattttc aacacagctt actctgtagc 480

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aaaatgtatc agtataggat ttagaatctc catgttgaaa ctctaaatgc atagaaataa 600

aaataataaa aaatttttca ttttggcttt tcagcctagt attaaaactg ataaaagcaa 660

agccatgcac aaaactacct ccctagagaa aggctagtcc cttttcttcc ccattcattt 720

catt atg aac ata gta gaa aac agc ata ttc tta tca aat ttg atg 766
Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met
1 5 10

aaa agc gcc aac acg ttt gaa ctg aaa tac gac ttg tca tgt gaa ctg 814
Lys Ser Ala Asn Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu
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Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser
35 40 45

gaa agg agt ctt gct cgt gct ggt ttc tat tac act ggt gtg aat gac 910
Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp
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aag gtc aaa tgc ttc tgt tgt ggc ctg atg ctg gat aac tgg aaa aga 958
Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg
65 70 75

gga gac agt cct act gaa aag cat aaa aag ttg tat cct agc tgc aga 1006
Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg
80 85 90

ttc gtt cag agt cta aat tcc gtt aac aac ttg gaa gct acc tct cag 1054
Phe Val Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln

95 100 105 110

cct act ttt cct tct tca gta aca aat tcc aca cac tca tta ctt ccg 1102
Pro Thr Phe Pro Ser Ser Val Thr Asn Ser Thr His Ser Leu Leu Pro
115 120 125

ggt aca gaa aac agt gga tat ttc cgt ggc tct tat tca aac tct cca 1150
Gly Thr Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro
130 135 140

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Ser Asn Pro Val Asn Ser Arg Ala Asn Gln Asp Phe Ser Ala Leu Met
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aga agt tcc tac cac tgt gca atg aat aac gaa aat gcc aga tta ctt 1246
Arg Ser Ser Tyr His Cys Ala Met Asn Asn Glu Asn Ala Arg Leu Leu
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act ttt cag aca tgg cca ttg act ttt ctg tcg cca aca gat ctg gca 1294
Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala
175 180 185 190

aaa gca ggc ttt tac tac ata gga cct gga gac aga gtg gct tgc ttt 1342
Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe
195 200 205

gcc tgt ggt gga aaa ttg agc aat tgg gaa ccg aag gat aat gct atg 1390
Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met
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tca gaa cac ctg aga cat ttt ccc aaa tgc cca ttt ata gaa aat cag 1438
Ser Glu His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln
225 230 235

ctt caa gac act tca aga tac aca gtt tct aat ctg agc atg cag aca 1486
Leu Gln Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr
240 245 250

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His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
255 260 265 270

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Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
275 280 285

agt gat gat gtc aaa tgc ttt tgc tgt gat ggt gga ctc agg tgt tgg 1630
Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
290 295 300

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Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
305 310 315

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Cys Glu Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val
320 325 330

caa gcc agt tac cct cat cta ctt gaa cag ctg cta tcc aca tca gac 1774
Gln Ala Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp
335 340 345 350

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Ser Pro Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Phe Glu Pro
355 360 365

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Gly Glu Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile
370 375 380

aat gct gcc gtg gaa atg ggc ttt agt aga agc ctg gta aaa cag aca 1918
Asn Ala Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr
385 390 395

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Val Gln Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn
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415 420 425 430

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Glu Arg Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu
435 440 445

atc cgg aag aat aga atg gca ctt ttt caa cat ttg act tgt gta att 2110
Ile Arg Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile
450 455 460

cca atc ctg gat agt cta cta act gcc gga att att aat gaa caa gaa 2158
Pro Ile Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu

465 470 475

cat gat gtt att aaa cag aag aca cag acg tct tta caa gca aga gaa 2206
His Asp Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu
480 485 490

ctg att gat acg att tta gta aaa gga aat att gca gcc act gta ttc 2254
Leu Ile Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe
495 500 505 510

aga aac tct ctg caa gaa gct gaa gct gtg tta tat gag cat tta ttt 2302
Arg Asn Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe
515 520 525

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Val Gln Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu
530 535 540

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545 550 555

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575 580 585 590

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Cys Arg Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600 605

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cccccgcccc ccggagctgc caacattgcc aacgccaccg ccacgctaca cacagcctca 180

actttcagga gacccgtccg tggccttatt tattccaccc ttcctgtaca tcgtagcgaa 240

tcaatccgtg gcgccgcact cctccgcatc cctctttaac agtacccctg ggatggcgtg 300

agcactcccc cagcg atg gac cca tct gtg acg ctg tgg cag ttt ctg 348
Met Asp Pro Ser Val Thr Leu Trp Gln Phe Leu
1 5 10

ctg cag ctg ctg aga gag caa ggc aat ggc cac atc atc tcc tgg act 396
Leu Gln Leu Leu Arg Glu Gln Gly Asn Gly His Ile Ile Ser Trp Thr

15 20 25

tca cgg gat ggt ggt gaa ttc aag ctg gtg gat gca gag gag gtg gcc 444
Ser Arg Asp Gly Gly Glu Phe Lys Leu Val Asp Ala Glu Glu Val Ala
30 35 40

cgg ctg tgg gga cta cgc aag aac aag acc aac atg aat tac gac aag 492
Arg Leu Trp Gly Leu Arg Lys Asn Lys Thr Asn Met Asn Tyr Asp Lys
45 50 55

ctc agc cgg gcc ttg cgg tac tac tat gac aag aac atc atc cgc aag 540
Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile Arg Lys
60 65 70 75

gtg agc ggc cag aag ttc gtc tac aag ttt gtg tcc tac cct gag gtc 588
Val Ser Gly Gln Lys Phe Val Tyr Lys Phe Val Ser Tyr Pro Glu Val
80 85 90

gca ggg tgc tcc act gag gac tgc ccg ccc cag cca gag gtg tct gtt 636
Ala Gly Cys Ser Thr Glu Asp Cys Pro Pro Gln Pro Glu Val Ser Val
95 100 105

acc tcc acc atg cca aat gtg gcc cct gct gct ata cat gcc gcc cca 684
Thr Ser Thr Met Pro Asn Val Ala Pro Ala Ala Ile His Ala Ala Pro
110 115 120

ggg gac act gtc tct gga aag cca ggc aca ccc aag ggt gca gga atg 732
Gly Asp Thr Val Ser Gly Lys Pro Gly Thr Pro Lys Gly Ala Gly Met
125 130 135

gca ggc cca ggc ggt ttg gca cgc agc agc cgg aac gag tac atg cgc 780
Ala Gly Pro Gly Gly Leu Ala Arg Ser Ser Arg Asn Glu Tyr Met Arg
140 145 150 155

tcg ggc ctc tat tcc acc ttc acc atc cag tct ctg cag ccg cag cca 828
Ser Gly Leu Tyr Ser Thr Phe Thr Ile Gln Ser Leu Gln Pro Gln Pro
160 165 170

ccc cct cat cct cgg cct gct gtg gtg ctc ccc aat gca gct cct gca 876
Pro Pro His Pro Arg Pro Ala Val Val Leu Pro Asn Ala Ala Pro Ala
175 180 185

ggg gca gca gcg ccc ccc tcg ggg agc agg agc acc agt cca agc ccc 924
Gly Ala Ala Ala Pro Pro Ser Gly Ser Arg Ser Thr Ser Pro Ser Pro
190 195 200

ttg gag gcc tgt ctg gag gct gaa gag gcc ggc ttg cct ctg cag gtc 972
Leu Glu Ala Cys Leu Glu Ala Glu Glu Ala Gly Leu Pro Leu Gln Val
205 210 215

atc ctg acc ccg ccc gag gcc cca aac ctg aaa tcg gaa gag ctt aat 1020
Ile Leu Thr Pro Pro Glu Ala Pro Asn Leu Lys Ser Glu Glu Leu Asn
220 225 230 235

gtg gag ccg ggt ttg ggc cgg gct ttg ccc cca gaa gtg aaa gta gaa 1068
Val Glu Pro Gly Leu Gly Arg Ala Leu Pro Pro Glu Val Lys Val Glu
240 245 250

ggg ccc aag gaa gag ttg gaa gtt gcg ggg gag aga ggg ttt gtg cca 1116
Gly Pro Lys Glu Glu Leu Glu Val Ala Gly Glu Arg Gly Phe Val Pro
255 260 265

gaa acc acc aag gcc gag cca gaa gtc cct cca cag gag ggc gtg cca 1164
Glu Thr Thr Lys Ala Glu Pro Glu Val Pro Pro Gln Glu Gly Val Pro
270 275 280

gcc cgg ctg ccc gcg gtt gtt atg gac acc gca ggg cag gcg ggc ggc 1212
Ala Arg Leu Pro Ala Val Val Met Asp Thr Ala Gly Gln Ala Gly Gly
285 290 295

cat gcg gct tcc agc cct gag atc tcc cag ccg cag aag ggc cgg aag 1260
His Ala Ala Ser Ser Pro Glu Ile Ser Gln Pro Gln Lys Gly Arg Lys
300 305 310 315

ccc cgg gac cta gag ctt cca ctc agc ccg agc ctg cta ggt ggg ccg 1308
Pro Arg Asp Leu Glu Leu Pro Leu Ser Pro Ser Leu Leu Gly Gly Pro
320 325 330

gga ccc gaa cgg acc cca gga tcg gga agt ggc tcc ggc ctc cag gct 1356
Gly Pro Glu Arg Thr Pro Gly Ser Gly Ser Gly Ser Gly Leu Gln Ala
335 340 345

ccg ggg ccg gcg ctg acc cca tcc ctg ctt cct acg cat aca ttg acc 1404
Pro Gly Pro Ala Leu Thr Pro Ser Leu Leu Pro Thr His Thr Leu Thr
350 355 360

ccg gtg ctg ctg aca ccc agc tcg ctg cct cct agc att cac ttc tgg 1452
Pro Val Leu Leu Thr Pro Ser Ser Leu Pro Pro Ser Ile His Phe Trp
365 370 375

agc acc ctg agt ccc att gcg ccc cgt agc ccg gcc aag ctc tcc ttc 1500
Ser Thr Leu Ser Pro Ile Ala Pro Arg Ser Pro Ala Lys Leu Ser Phe

380 385 390 395

cag ttt cca tcc agt ggc agc gcc cag gtg cac atc cct tct atc agc 1548
Gln Phe Pro Ser Ser Gly Ser Ala Gln Val His Ile Pro Ser Ile Ser
400 405 410

gtg gat ggc ctc tcg acc ccc gtg gtg ctc tcc cca ggg ccc cag aag 1596
Val Asp Gly Leu Ser Thr Pro Val Val Leu Ser Pro Gly Pro Gln Lys
415 420 425

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cagcctgccc ttggggagat gagggagccc tgtctgcgtt tttggatgtg agtagaagag 2072

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atttaatggg ttgggagtct tggccaagga agaatcacac ccttggaata gaaatttcca 2192

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Glu Ser Lys Arg Ile Asn Ala Glu Ile Glu Lys Gln Leu Arg Arg Asp
20 25 30

aag cgc gac gcc cgg cgc gag ctc aag ctg ctg ctg ctc ggc acg ggc 144
Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly
35 40 45

gag agc ggg aag agc acg ttc atc aag cag atg cgc atc atc cac ggc 192
Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
50 55 60

gcc ggc tac tcg gag gag gac aag cgc ggc ttc acc aag ctc gtc tac 240
Ala Gly Tyr Ser Glu Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
65 70 75 80

cag aac atc ttc acc gcc atg cag gcc atg atc cgg gcc atg gag acg 288
Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Glu Thr
85 90 95

ctc aag atc ctc tac aag tac gag cag aac aag gcc aat gcg ctc ctg 336
Leu Lys Ile Leu Tyr Lys Tyr Glu Gln Asn Lys Ala Asn Ala Leu Leu
100 105 110

atc cgg gag gtg gac gtg gag aag gtg acc acc ttc gag cat cag tac 384
Ile Arg Glu Val Asp Val Glu Lys Val Thr Thr Phe Glu His Gln Tyr
115 120 125

gtc agt gcc atc aag acc ctg tgg gag gac ccg ggc atc cag gaa tgc 432
Val Ser Ala Ile Lys Thr Leu Trp Glu Asp Pro Gly Ile Gln Glu Cys
130 135 140

tac gac cgc agg cgc gag tac cag ctc tcc gac tct gcc aag tac tac 480
Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr
145 150 155 160

ctg acc gac gtt gac cgc atc gcc acc ttg ggc tac ctg ccc acc cag 528
Leu Thr Asp Val Asp Arg Ile Ala Thr Leu Gly Tyr Leu Pro Thr Gln
165 170 175

cag gac gtg ctg cgg gtc cgc gtg ccc acc acc ggc atc atc gag tac 576
Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
180 185 190

cct ttc gac ctg gag aac atc atc ttc cgg atg gtg gat gtg ggg ggc 624
Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly
195 200 205

cag cgg tcg gag cgg agg aag tgg atc cac tgc ttt gag aac gtg aca 672
Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr
210 215 220

tcc atc atg ttt ctc gtc gcc ctc agc gaa tac gac caa gtc ctg gtg 720
Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val
225 230 235 240

gag tcg gac aac gag aac cgg atg gag gag agc aaa gcc ctg ttc cgg 768
Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg
245 250 255

acc atc atc acc tac ccc tgg ttc cag aac tcc tcc gtc atc ctc ttc 816
Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe
260 265 270

ctc aac aag aag gac ctg ctg gag gac aag atc ctg tac tcg cac ctg 864
Leu Asn Lys Lys Asp Leu Leu Glu Asp Lys Ile Leu Tyr Ser His Leu
275 280 285

gtg gac tac ttc ccc gag ttc gat ggt ccc cag cgg gac gcc cag gcg 912
Val Asp Tyr Phe Pro Glu Phe Asp Gly Pro Gln Arg Asp Ala Gln Ala
290 295 300

gcg cgg gag ttc atc ccg aag atg ttc gtg gac ctg aac ccc gac agc 960
Ala Arg Glu Phe Ile Pro Lys Met Phe Val Asp Leu Asn Pro Asp Ser
305 310 315 320

gac aag atc atc tac tca cac ttc acg tgt gcc acc gac acg gag aac 1008
Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn

325 330 335

atc cgc ttc gtg ttc gcg gcc gtg aag gac acc atc ctg cag ctg aac 1056
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gcgggagcct cgggcacc atg agc gac gtg gct att gtg aag gag ggt tgg 231
Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp
1 5 10

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Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe
15 20 25

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Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln
30 35 40

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Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln
45 50 55

tgc cag ctg atg aag acg gag cgg ccc cgg ccc aac acc ttc atc atc 423
Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile
60 65 70 75

cgc tgc ctg cag tgg acc act gtc atc gaa cgc acc ttc cat gtg gag 471
Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His Val Glu
80 85 90

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Thr Pro Glu Glu Arg Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala
95 100 105

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Asp Gly Leu Lys Lys Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly

110 115 120

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Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala
125 130 135

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Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu
140 145 150 155

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160 165 170

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Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val
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gcc aag gac gag gtg gcc cac aca ctc acc gag aac cgc gtc ctg cag 807
Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln
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Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr
205 210 215

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His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu
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Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg
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270 275 280

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Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr
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Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu
365 370 375

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Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro
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Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr
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445 450 455

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Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser
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Ala Ser Ser Thr Ala

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